REMARKS

Entry of this Preliminary Amendment is believed to be proper and is respectfully requested. The Amendment was necessitated by corrections to the Sequence Listing in response to a Notice to Comply with sequence listing requirements mailed on June 19, 2002.

By this Amendment, the Specification and the Figures have been amended to insert the newly added SEQ ID NOs. No new matter has been added.

A set of amended Formal Drawings is enclosed as a replacement for the informal drawings submitted with the Specification. A Petition to accept color drawings under 1.84(a)(2), and the required fee, accompanies this Amendment.

Applicant submits that this application is now in condition for allowance, and an early favorable response is respectfully requested.

Respectfully submitted,

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Sept. 10/02

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Version with markings to show change made

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IN THE FIGURES:

A marked-up version of the amendments to the Figures, with changes indicated in RED underlining is enclosed. The amended Formal Drawings are submitted as the clean copy incorporating the amendments.

N THE SPECIFICATION:

At page 2, line 25, please replace the paragraph beginning "Figure 1:" with the following paragraph:

Figure 1: The inversion sequence of the apo-dystrophin-4 cDNA. A cryptic polyadenylation site is underlined at +990. The four peptides coded for by the sequence are SEQ ID NOs: 34, 35, 36, and 37, respectively.

At page 3, line 4, please replace the paragraph beginning "Figure 2:" with the following paragraph:

Figure 2: The polynucleotide sequence of apo-dystrophin-4. The inversion sequence shown in Figure 1 begins at base pair 860 and ends at base pair 996. The sixteen peptides coded for by the entire sequence are SEQ ID NOs: 38 through 50 and 35 through 37, respectively.

At page 3, line 26, please replace the entire paragraph beginning "Figure 6:" with the following paragraph:

Figure 6: **The full-length apo-dystrophin-4 cDNA and upstream genomic sequence translated.** Genomic sequence upstream of the apo-dystrophin-4 cDNA is shown from -233 to -1, the start of the apo-4 sequence. (SEQ ID NO: 51). The peptides coded for by the sequence are listed as SEQ ID NOs: 52, 53, 38-50 and 35-37, respectively. The sequence was subjected to a MacVector alignment and was homologous with the 3' end of the dystrophin cDNA, up until the inversion at 860. A search of the 3' 137 bp of apo-4 alone showed that it was precisely

homologous to 3' dystrophin sequence 1.62 Kb downstream in the 3' UTR in the reverse orientation and was thus an inversion of the 3' UTR and genomic sequence. Three potential starting methionines are highlighted at +25, +88, and +100. and a potential CAAT box is underlined at +57. These M's are in phase I of apo-4 alone, but appear in phase II here due to the presence of upstream sequence. The longest open reading frame that should be obtainable from this sequence begins with the M at +88 (33aa). The beginning of exon 79 at 453 is also underlined. For a predicted protein in frame 2, a putative transmembrane domain is underlined and putative N-glycosylation sites that follow the Asn-Xxx-Ser/Thr motif are shown (in parentheses when utilized if nonsense suppression occurs). A cryptic polyadenylation site is underlined at +990. The upstream exon identified by GRAIL appears from -90 to -5.